

05-90
0322

#2



OIPE

RAW SEQUENCE LISTING

DATE: 03/26/2002

PATENT APPLICATION: US/10/033,109

TIME: 09:33:25

Input Set : N:\Crf3\RULE60\10033109.raw

Output Set: N:\CRF3\03262002\J033109.raw

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1 <110> APPLICANT: Allen, Stephen M.
2   Rafalski, J. Antoni
3   Sakai, Hajime
4 <120> TITLE OF INVENTION: Nitrogen Transport Metabolism
5 <130> FILE REFERENCE: BB-1210
6 <140> CURRENT APPLICATION NUMBER: 10/033,109
7 <141> CURRENT FILING DATE: 2001-12-28
10 <150> PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/384,625
W--> 11 <151> PRIOR FILING DATE: EARLIER FILING DATE: 1999-08-27
13 <150> PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/098,248
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21 <213> ORGANISM: Zea mays
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25   ggttcgacga cccgctggag gcggcgcgagc tgacggcgcg gtgtggcgcc tggggcgctc   180
26   tcttcacggg gctcttcgcg aggcgaaagt acgtggagga gatctacggc gccgggagggc   240
27   cctacgggct gtccatgggc ggcggcggga agctcctcgc cgcgcagatc atccagatcc   300
28   tgggtatcgc cgggtgggtg agctgcacca tgggcccgct cttctacgcy ctcaagaagc   360
29   tgggcctgct gcgcattctg gccgacgacg agatgtccgg catggacctg acccggcacg   420
30   gcggcttcgc ctacgtctac cacgacgagg accctggcga caaggccggg gttggtgggt   480
31   tcatgtcaa gtccgcgcag aaccgtgtcg agccggcggc ggcggtggcg gcggcgacca   540
32   gcagccaggt gtaaaaaaaaa aatcaggagc aaattgaaac cgagctgaag ttacgtgctt   600
33   gccttttttc gtatgttgct gcgtatcacg tttgaggtgg atcgtatctg ccggtcagta   660
34   cgcagtgttt gggcaaatat ttggctactt gggagtcgca agaaattgtg taaattatat   720
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ENTERED

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53   Gln Leu His Gly Gly Cys Gly Ala Trp Gly Val Leu Phe Thr Gly Leu
54           50                55                60
55   Phe Ala Arg Arg Lys Tyr Val Glu Glu Ile Tyr Gly Ala Gly Arg Pro
56           65                70                75                80
57   Tyr Gly Leu Phe Met Gly Gly Gly Gly Lys Leu Leu Ala Ala Gln Ile
58           85                90                95
59   Ile Gln Ile Leu Val Ile Ala Gly Trp Val Ser Cys Thr Met Gly Pro
60           100               105               110
61   Leu Phe Tyr Ala Leu Lys Lys Leu Gly Leu Leu Arg Ile Ser Ala Asp
62           115               120               125
63   Asp Glu Met Ser Gly Met Asp Leu Thr Arg His Gly Gly Phe Ala Tyr
64           130               135               140
65   Val Tyr His Asp Glu Asp Pro Gly Asp Lys Ala Gly Val Gly Gly Phe
66           145               150               155               160
67   Met Leu Lys Ser Ala Gln Asn Arg Val Glu Pro Ala Ala Ala Val Ala
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73 <211> LENGTH: 1706
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75 <213> ORGANISM: Glycine max
76 <400> SEQUENCE: 3
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78   ctaaccaacc caccatgtcg ctgcctgctt gtcccgccga acaactggcc caacttctcg 120
79   gcccaaacac cacagaagcc cccgcgcgcg cctcccttat ctgcggccat ttgcgcgcgc 180
80   tggacagcaa gttcgtcgac acggccttcg ccgtcgacaa cacctacctc ctcttttccg 240
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82   ccaagaacac catgaacatc atgtcacca acgtcctgga cgctgccgcc ggcggcctct 360
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84   aacatttctt cggcctcaag gacatccctt catcctccta cgactacagc tacttctctt 480
85   accaatgggc cttcgccatc gccgcgcgcg gcatcaccag cggaagcatc gccgaacgca 540
86   cacagttcgt ggcctatctc atctactcct ccttcctcac cggcttcgtc tatccggtgg 600
87   tctcccaactg gttctggtcc ccagacggct gggcctctgc ctttaagatc accgaccggc 660
88   tattttccac cggcgtaata gacttcgcgc gttccggcgt agtccacatg gtcggcggaa 720
89   tagccggcct atggggagcg ctgatcgaag gcccaagaat gggacgtttc gatcatgcag 780
90   gacgagctgt ggccttgcca ggccacagcg cgtccttagt agtccctgga accttcttgc 840
91   tttggttcgg ttggtacgga ttttaacccg gtccatttaa caaaatccta cttacttaac 900
92   gtaactcagg aaattactac ggtcaatgga gcgcggttg cagaaccgcg gtcaccacta 960
93   ccctagcggg gtcaacagct gccttgacca cgctattcgg taaacgggtg atatccggtc 1020
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95   gttgctcgtt ggttgagcca tgggcagcca tcgtatgcgg ttttggtgct tctatagtat 1140
96   taatagcttg caacaaatta gcagagaagg ttaagttcga cgatcctctg gaggcggcgc 1200
97   agttgcacgg tgggtgtggc acgtgggggg tgatattcac ggcgttggtc gcaaaaaagg 1260
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Output Set: N:\CRF3\03262002\J033109.raw

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101     atgagcttgc ggggatggac atgactcgcc atggaggctt tgcttatgct tatgaggatg 1500
102     atgagacgca caagcatggg atgcagttga ggagggttgg gcccacgcg tcttcacac 1560
103     ccaccactga tgaatgatct tttttccca tatgcatgct tcattagtca aacattaat 1620
104     ttggatacat attccttgta aggattcaaa ccttggttac ttgttacttc tgtaaaaaa 1680
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111 <400> SEQUENCE: 4
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115             20             25             30
116     Phe Ala Ala Val Asp Ser Lys Phe Val Asp Thr Ala Phe Ala Val Asp
117             35             40             45
118     Asn Thr Tyr Leu Leu Phe Ser Ala Tyr Leu Val Phe Ser Met Gln Leu
119             50             55             60
120     Gly Phe Ala Met Leu Cys Ala Gly Ser Val Arg Ala Lys Asn Thr Met
121             65             70             75             80
122     Asn Ile Met Leu Thr Asn Val Leu Asp Ala Ala Gly Gly Leu Phe
123             85             90             95
124     Tyr Tyr Leu Phe Gly Phe Ala Phe Ala Phe Gly Ser Pro Ser Asn Gly
125             100            105            110
126     Phe Ile Gly Lys His Phe Phe Gly Leu Lys Asp Ile Pro Ser Ser Ser
127             115            120            125
128     Tyr Asp Tyr Ser Tyr Phe Leu Tyr Gln Trp Ala Phe Ala Ile Ala Ala
129             130            135            140
130     Ala Gly Ile Thr Ser Gly Ser Ile Ala Glu Arg Thr Gln Phe Val Ala
131             145            150            155            160
132     Tyr Leu Ile Tyr Ser Ser Phe Leu Thr Gly Phe Val Tyr Pro Val Val
133             165            170            175
134     Ser His Trp Phe Trp Ser Pro Asp Gly Trp Ala Ser Ala Phe Lys Ile
135             180            185            190
136     Thr Asp Arg Leu Phe Ser Thr Gly Val Ile Asp Phe Ala Gly Ser Gly
137             195            200            205
138     Val Val His Met Val Gly Gly Ile Ala Gly Leu Trp Gly Ala Leu Ile
139             210            215            220
140     Glu Gly Pro Arg Met Gly Arg Phe Asp His Ala Gly Arg Ala Val Ala
141             225            230            235            240
142     Leu Arg Gly His Ser Ala Ser Leu Val Val Leu Gly Thr Phe Leu Leu
143             245            250            255
144     Trp Phe Gly Trp Tyr Gly Phe Asn Pro Gly Ser Phe Asn Lys Ile Leu
145             260            265            270
146     Leu Thr Tyr Gly Asn Ser Gly Asn Tyr Tyr Gly Gln Trp Ser Ala Val
147             275            280            285
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Output Set: N:\CRF3\03262002\J033109.raw

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152	Asp Val Cys Asn Gly Leu Leu Gly Gly Phe Ala Ala Ile Thr Ala Gly		
153		325	330
154	Cys Ser Val Val Glu Pro Trp Ala Ala Ile Val Cys Gly Phe Val Ala		
155		340	345
156	Ser Ile Val Leu Ile Ala Cys Asn Lys Leu Ala Glu Lys Val Lys Phe		
157		355	360
158	Asp Asp Pro Leu Glu Ala Ala Gln Leu His Gly Gly Cys Gly Thr Trp		
159		370	375
160	Gly Val Ile Phe Thr Ala Leu Phe Ala Lys Lys Glu Tyr Val Lys Glu		
161		385	390
162	Val Tyr Gly Leu Gly Arg Ala His Gly Leu Leu Met Gly Gly Gly Gly		
163		405	410
164	Lys Leu Leu Ala Ala His Val Ile Gln Ile Leu Val Ile Ala Gly Trp		
165		420	425
166	Val Ser Ala Thr Met Gly Pro Leu Phe Trp Gly Leu Asn Lys Leu Lys		
167		435	440
168	Leu Leu Arg Ile Ser Ser Glu Asp Glu Leu Ala Gly Met Asp Met Thr		
169		450	455
170	Arg His Gly Gly Phe Ala Tyr Ala Tyr Glu Asp Asp Glu Thr His Lys		
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172	His Gly Met Gln Leu Arg Arg Val Gly Pro Asn Ala Ser Ser Thr Pro		
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184	ggcgaacgcc acggactacc tgtgcaacag gttcgccgac accacgtccg cggaggactc 180		
185	cacctacctg ctcttctcgg cctacctcgt cttcgccatg cagctcggct tcgcatgct 240		
186	ctgcgcgggc tccgtccggg ccaagaacac catgaacatc atgctcacca acgtgctcga 300		
187	cgccgcggcc ggcgcgctct tctactacct cttcggttcc gccttcgctt tcgggacgcc 360		
188	gtcgaacggc ttcacgcgga agcacttctt cggcctcaag gacatgccgc agaccggctt 420		
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192	ggcccgacag tccggccgcg tgctcttcaa gtccggcgtg atcgacttcg ccggctccgg 660		
193	cgtcgtgcac atggtcggcg gcatcgccgg cttctggggc gcgtccatcg agggcccccg 720		
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196	cgtcaccatc ctcaagtcgt acggcccgcc cgggagcatc aacgggcagt ggtcgggcgt 900		
197	gggcgcgacc gccgtgacga cgaagctggc gggcagcgtg gcggcgctca cgacgctgtt 960		
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PATENT APPLICATION: US/10/033,109

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TIME: 09:33:26

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201 cgacgaccg ctggaggcgg cgcagctgca cggcggctgc ggcgcgctgg ggatcatctt 1200
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205 cctgctccgc atctcggccg aggacgagat ggccggcatg gacctgacct ggcacgggtg 1440
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207 caggtcggcg cagaccgcg tcgagccggc ggccggcgcg aacagccagg tctaaccaat 1560
208 caagccggac tacgtaacaa gaaatccagt ggaaatcgcc tttctgttct cgcgcgtcat 1620
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210 ggcgctcttg tgttcgttca caagattgta aaattattac actaggacga ggttattttt 1740
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213 tgatcatgag ggtgtggtca agatagggtg ctgctcaagg ttgaattgtt gagatttgct 1920
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215 aaaaaaaaaa a 1991
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225 20 25 30
226 Ser Ala Val Asp Ser Thr Tyr Leu Leu Phe Ser Ala Tyr Leu Val Phe
227 35 40 45
228 Ala Met Gln Leu Gly Phe Ala Met Leu Cys Ala Gly Ser Val Arg Ala
229 50 55 60
230 Lys Asn Thr Met Asn Ile Met Leu Thr Asn Val Leu Asp Ala Ala Ala
231 65 70 75 80
232 Gly Ala Leu Phe Tyr Tyr Leu Phe Gly Phe Ala Phe Ala Phe Gly Thr
233 85 90 95
234 Pro Ser Asn Gly Phe Ile Gly Lys His Phe Phe Gly Leu Lys Asp Met
235 100 105 110
236 Pro Gln Thr Gly Phe Asp Tyr Ser Phe Phe Leu Phe Gln Trp Ala Phe
237 115 120 125
238 Ala Ile Ala Ala Ala Gly Ile Thr Ser Gly Ser Ile Ala Glu Arg Thr
239 130 135 140
240 Gln Phe Val Ala Tyr Leu Ile Tyr Ser Ala Phe Leu Thr Gly Phe Val
241 145 150 155 160
242 Tyr Pro Val Val Ser His Trp Ile Trp Ser Val Asp Gly Trp Ala Ser
243 165 170 175
244 Ala Ala Arg Thr Ser Gly Pro Leu Leu Phe Lys Ser Gly Val Ile Asp
245 180 185 190
246 Phe Ala Gly Ser Gly Val Val His Met Val Gly Gly Ile Ala Gly Phe
247 195 200 205
248 Trp Gly Ala Leu Ile Glu Gly Pro Arg Ile Gly Arg Phe Asp His Ala

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VERIFICATION SUMMARY

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Output Set: N:\CRF3\03262002\J033109.raw

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L:14 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD
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L:314 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:318 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:7
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